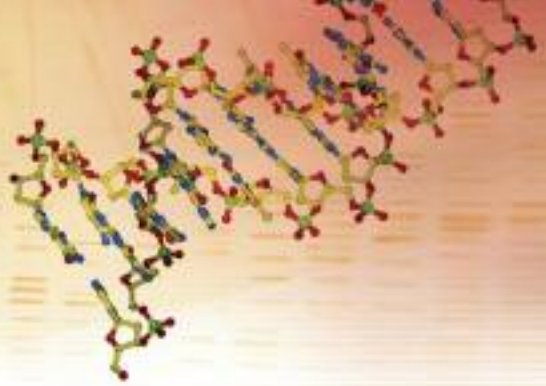
National Cancer Institute

OFFICE OF *CANCER GENOMICS*



MISSION AND GOALS

The National Cancer Institute's (NCI) Office of Cancer Genomics (OCG) seeks to enhance the understanding of the molecular mechanisms of cancer, with the ultimate goal of improving prevention, early detection, diagnosis, and treatment. Specifically, OCG fosters the application of genomics to cancer research by establishing information platforms, material resources, and technology infrastructure.

By advancing cancer genomics, OCG is paving the way for personalized medicine and enabling researchers throughout the world to develop a new generation of targeted diagnostics and therapies.

To accomplish its mission, OCG works to:

- Provide genomic information, technology, methods, informatics tools, and reagents to serve the cancer research community.
- Support, lead, and/or manage several major research programs, including:
  - Cancer Genetic Markers of Susceptibility
  - Cancer Genome Anatomy Project/Cancer Genome Characterization Initiative
  - Cancer Target Discovery and Development Network
  - NIH Mammalian Gene Collection
  - Therapeutically Applicable Research to Generate Effective Treatments
  - The Cancer Genome Atlas
- Establish and maintain relationships with advisory groups for each of its programs.

CANCER GENETIC MARKERS OF SUSCEPTIBILITY (CGEMS)

From a three-year pilot study in 2005, CGEMS has developed into a robust research program to identify common genetic variants that affect individual risk of developing cancer. Genome-wide association studies (GWAS) are conducted by NCI's Division of Cancer Epidemiology and Genetics in collaboration with extramural scientists. Common genetic variations identified through GWAS can help researchers trace the location of multiple inherited genes that predispose individuals to develop or resist cancer.

The data generated by CGEMS are made rapidly available through the CGEMS data access portal.

To learn more about CGEMS, visit *http://cgems.cancer.gov*.

CANCER GENOME ANATOMY PROJECT (CGAP)/CANCER GENOME CHARACTERIZATION INITIATIVE (CGCI)

CGAP provides the research community with an openly accessible online resource of genomic data characterizing normal, precancerous, and cancerous tissues. These data include gene expression profiles based on expressed sequence tags (EST) and serial analysis of gene expression (SAGE); single nucleotide polymorphism (SNP) analysis of cancer-related genes; and the Mitelman database of chromosomal aberrations in cancer (which contains >50,000 cases). Researchers can use CGAP analytical tools to analyze and compare SAGE data generated in their lab to CGAP data.

Building on CGAP, CGCI incorporates multiple genomic characterization methods including exome and transcriptome analysis using second-generation sequencing.

To learn more about CGAP and CGCI and to access the data generated by these initiatives, visit *http://cgap.nci.nih.gov*.

CANCER TARGET DISCOVERY AND DEVELOPMENT (CTD²) NETWORK

The CTD² Network aims to advance the development of novel approaches that will identify and validate therapeutic targets together with the diagnostic and stratification biomarkers from large-scale cancer genomic studies, such as the TARGET and TCGA initiatives. These multi-dimensional cancer genomic data sets reveal unprecedented detail in the driver mutations that lead to cancer. The integration of these data sets with biological information from basic research is providing new directions for developing individualized treatment strategies for cancer patients.

To learn more about CTD², visit *http://ocg.cancer.gov/programs/ctdd.asp*.

U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES

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MAMMALIAN GENE COLLECTION (MGC)

MGC is a resource for full-length open reading frame (FL-ORF) clones of mammalian genes. Completed in 2009, the MGC Project includes 17,502 human genes and 17,702 mouse genes. In total, 73,000 FL-ORFs are available, representing more than 50,000 unique genes from humans, mice, rats, and cows.

MGC infrastructure and protocols are also being applied to two other publicly accessible gene collection projects: *Xenopus laevis* and *Xenopus tropicalis* (frog), and *Danio rerio* (zebrafish).

To learn more about MGC, visit ***http://mgc.nci.nih.gov***.

THERAPEUTICALLY APPLICABLE RESEARCH TO GENERATE EFFECTIVE TREATMENTS (TARGET)

The TARGET Initiative harnesses the power of modern genomics tools for the identification of potential therapeutic targets in childhood cancers so that new, more effective treatments can be developed rapidly.

Funding from the American Recovery and Reinvestment Act has enabled NCI to expand TARGET research efforts from two to five cancers. TARGET is researching the genomic changes associated with acute lymphoblastic and myeloid leukemias, neuroblastoma, osteosarcoma, and Wilms tumor. The research comprises genomic characterization, gene sequencing, and RNA interference (RNAi), which forms a comprehensive system for selecting the most promising therapeutic targets.

To learn more about TARGET and the data it is producing to enable the development of targeted therapies for pediatric cancers, visit ***http://target.cancer.gov***.

THE CANCER GENOME ATLAS (TCGA)

TCGA aims to produce comprehensive genomic maps of at least 20 types of cancer. This pioneering effort to map and analyze cancer genomes in a large-scale, systematic manner will ultimately change the way cancer is detected and treated.

TCGA is uniquely positioned to achieve this ambitious goal through key infrastructure and processes that enable it to:

- Acquire tissue samples from a wide range of clinical sites.
- Efficiently extract genetic material from tissue samples.
- Rapidly characterize and sequence thousands of DNA and RNA samples.
- Collaboratively analyze and integrate diverse types of data.
- Swiftly report data through public databases designed to protect patient privacy.

TCGA data will enable both public and private sector researchers to pursue new detection and treatment strategies aimed at the specific pathways involved in a certain cancer type or subtype.

To learn more about TCGA, visit ***http://cancergenome.nih.gov***.

THE ROLE OF THE CANCER BIOMEDICAL INFORMATICS GRID (CABIG®)

Because all data generated through its programs are intended to be shared with the research community to accelerate discovery, OCG needs to ensure that the various forms and large amounts of data are easily accessible and interpretable. Thus, OCG is committed to the tools and infrastructure of caBIG® to achieve semantic interoperability. All data from OCG's programs are accessible through the extensive library of caBIG® programs and databases. OCG initiatives also utilize caBIG® analytical tools to enable researchers to explore the data for their own research efforts.

To learn more about caBIG®, visit ***https://cabig.nci.nih.gov***.

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CONTACT US:

FOR MORE INFORMATION ABOUT THE OFFICE OF CANCER GENOMICS, PLEASE CONTACT:

Office of Cancer Genomics

National Cancer Institute
Building 31, Room 10A07
31 Center Drive, MSC 2580
Bethesda, Maryland 20892-2580

Phone: (301) 451-8027
Fax: (301) 480-4368

E-mail: *ocg@mail.nih.gov*
Website: *http://ocg.cancer.gov*

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